RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10/594,339
Source: IFWP
Date Processed by STIC: 10/13/2006

ENTERED

CRF Errors Edited by the STIC Systems Branch

Serial Number: 10/594,339 **CRF Edit Date:** 10/13/2006
Edited by: DA

____ **Realigned nucleic acid/amino acid numbers/text in cases where the sequence text "wrapped" to the next line**

____ **Corrected the SEQ ID NO. Sequence numbers edited were:**

_____

____ **Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited:**

_____

____ **Deleted: ___ invalid beginning/end-of-file text ; ___ page numbers**

____ **Inserted mandatory headings/numeric identifiers, specifically:**

_____

____ **Moved responses to same line as heading/numeric identifier, specifically:**

_____

✓ **Other:** Moved the number up (1347)

Revised 09/09/2003

IFWP

RAW SEQUENCE LISTING DATE: 10/13/2006
PATENT APPLICATION: **US/10/594,339** TIME: 15:00:13

Input Set : A:\ptc.da.txt
Output Set: **N:\CRF4\10132006\J594339.raw**

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     3 <110> APPLICANT: Kyoto University
     5 <120> TITLE OF INVENTION: Cleaved forms of DANCE and DANCE complexes, and methods of
screening
     6       an agent for regulating formation of elastic fibre using them
W-->  8 <130> FILE REFERENCE:
C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/594,339
C--> 10 <141> CURRENT FILING DATE: 2006-09-27
     10 <150> PRIOR APPLICATION NUMBER: JP 2004-096685
W--> 11 <151> PRIOR FILING DATE: 2004-3-29
     13 <160> NUMBER OF SEQ ID NOS: 29
     15 <170> SOFTWARE: PatentIn version 3.2
     17 <210> SEQ ID NO: 1
     18 <211> LENGTH: 1347
     19 <212> TYPE: DNA
     20 <213> ORGANISM: Homo sapiens
     23 <220> FEATURE:
     24 <221> NAME/KEY: CDS
     25 <222> LOCATION: (1)..(1347)
     27 <400> SEQUENCE: 1
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     29 Met Pro Gly Ile Lys Arg Ile Leu Thr Val Thr Ile Leu Ala Leu Cys
     30 1               5                  10                  15
     32 ctt cca agc cct ggg aat gca cag gca cag tgc acg aat ggc ttt gac       96
     33 Leu Pro Ser Pro Gly Asn Ala Gln Ala Gln Cys Thr Asn Gly Phe Asp
     34             20                  25                  30
     36 ctg gat cgc cag tca gga cag tgt tta gat att gat gaa tgc cga acc      144
     37 Leu Asp Arg Gln Ser Gly Gln Cys Leu Asp Ile Asp Glu Cys Arg Thr
     38         35                  40                  45
     40 atc ccc gag gcc tgc cga gga gac atg atg tgt gtt aac caa aat ggc      192
     41 Ile Pro Glu Ala Cys Arg Gly Asp Met Met Cys Val Asn Gln Asn Gly
     42     50                  55                  60
     44 ggg tat tta tgc att ccc cgg aca aac cct gtg tat cga ggg ccc tac      240
     45 Gly Tyr Leu Cys Ile Pro Arg Thr Asn Pro Val Tyr Arg Gly Pro Tyr
     46 65                  70                  75                  80
     48 tcg aac ccc tac tcg acc ccc tac tca ggt ccg tac cca gca gct gcc      288
     49 Ser Asn Pro Tyr Ser Thr Pro Tyr Ser Gly Pro Tyr Pro Ala Ala Ala
     50                 85                  90                  95
     52 cca cca ctc tca gct cca aac tat ccc acg atc tcc agg cct ctt ata      336
     53 Pro Pro Leu Ser Ala Pro Asn Tyr Pro Thr Ile Ser Arg Pro Leu Ile
     54             100                 105                 110
     56 tgc cgc ttt gga tac cag atg gat gaa agc aac caa tgt gtg gat gtg      384
     57 Cys Arg Phe Gly Tyr Gln Met Asp Glu Ser Asn Gln Cys Val Asp Val
     58         115                 120                 125
     60 gac gag tgt gca aca gat tcc cac cag tgc aac ccc acc cag atc tgc      432
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RAW SEQUENCE LISTING DATE: 10/13/2006
PATENT APPLICATION: US/10/594,339 TIME: 15:00:13

Input Set : A:\pto.da.txt
Output Set: N:\CRF4\10132006\J594339.raw

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61 Asp Glu Cys Ala Thr Asp Ser His Gln Cys Asn Pro Thr Gln Ile Cys
62     130                 135                 140
64 atc aat act gaa ggc ggg tac acc tgc tcc tgc acc gac gga tat tgg      480
65 Ile Asn Thr Glu Gly Gly Tyr Thr Cys Ser Cys Thr Asp Gly Tyr Trp
66 145                 150                 155                 160
68 ctt ctg gaa ggc cag tgc tta gac att gat gaa tgt cgc tat ggt tac      528
69 Leu Leu Glu Gly Gln Cys Leu Asp Ile Asp Glu Cys Arg Tyr Gly Tyr
70                 165                 170                 175
72 tgc cag cag ctc tgt gcg aat gtt cct gga tcc tat tct tgt aca tgc      576
73 Cys Gln Gln Leu Cys Ala Asn Val Pro Gly Ser Tyr Ser Cys Thr Cys
74             180                 185                 190
76 aac cct ggt ttt acc ctc aat gag gat gga agg tct tgc caa gat gtg      624
77 Asn Pro Gly Phe Thr Leu Asn Glu Asp Gly Arg Ser Cys Gln Asp Val
78         195                 200                 205
80 aac gag tgt gcc acc gag aac ccc tgc gtg caa acc tgc gtc aac acc      672
81 Asn Glu Cys Ala Thr Glu Asn Pro Cys Val Gln Thr Cys Val Asn Thr
82     210                 215                 220
84 tac ggc tct ttc atc tgc cgc tgt gac cca gga tat gaa ctt gag gaa      720
85 Tyr Gly Ser Phe Ile Cys Arg Cys Asp Pro Gly Tyr Glu Leu Glu Glu
86 225                 230                 235                 240
88 gat ggc gtt cat tgc agt gat atg gac gag tgc agc ttc tct gag ttc      768
89 Asp Gly Val His Cys Ser Asp Met Asp Glu Cys Ser Phe Ser Glu Phe
90                 245                 250                 255
92 ctc tgc caa cat gag tgt gtg aac cag ccc ggc aca tac ttc tgc tcc      816
93 Leu Cys Gln His Glu Cys Val Asn Gln Pro Gly Thr Tyr Phe Cys Ser
94             260                 265                 270
96 tgc cct cca ggc tac atc ctg ctg gat gac aac cga agc tgc caa gac      864
97 Cys Pro Pro Gly Tyr Ile Leu Leu Asp Asp Asn Arg Ser Cys Gln Asp
98         275                 280                 285
100 atc aac gaa tgt gag cac agg aac cac acg tgc aac ctg cag cag acg      912
101 Ile Asn Glu Cys Glu His Arg Asn His Thr Cys Asn Leu Gln Gln Thr
102     290                 295                 300
104 tgc tac aat tta caa ggg ggc ttc aaa tgc atc gac ccc atc cgc tgt      960
105 Cys Tyr Asn Leu Gln Gly Gly Phe Lys Cys Ile Asp Pro Ile Arg Cys
106 305                 310                 315                 320
108 gag gag cct tat ctg agg atc agt gat aac cgc tgt atg tgt cct gct     1008
109 Glu Glu Pro Tyr Leu Arg Ile Ser Asp Asn Arg Cys Met Cys Pro Ala
110                 325                 330                 335
112 gag aac cct ggc tgc aga gac cag ccc ttt acc atc ttg tac cgg gac     1056
113 Glu Asn Pro Gly Cys Arg Asp Gln Pro Phe Thr Ile Leu Tyr Arg Asp
114             340                 345                 350
116 atg gac gtg gtg tca gga cgc tcc gtt ccc gct gac atc ttc caa atg     1104
117 Met Asp Val Val Ser Gly Arg Ser Val Pro Ala Asp Ile Phe Gln Met
118         355                 360                 365
120 caa gcc acg acc cgc tac cct ggg gcc tat tac att ttc cag atc aaa     1152
121 Gln Ala Thr Thr Arg Tyr Pro Gly Ala Tyr Tyr Ile Phe Gln Ile Lys
122     370                 375                 380
124 tct ggg aat gag ggc aga gaa ttt tac atg cgg caa acg ggc ccc atc     1200
125 Ser Gly Asn Glu Gly Arg Glu Phe Tyr Met Arg Gln Thr Gly Pro Ile
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RAW SEQUENCE LISTING DATE: 10/13/2006
PATENT APPLICATION: US/10/594,339 TIME: 15:00:13

Input Set : A:\pto.da.txt
Output Set: N:\CRF4\10132006\J594339.raw

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126 385                 390                 395                 400
128 agt gcc acc ctg gtg atg aca cgc ccc atc aaa ggg ccc cgg gaa atc     1248
129 Ser Ala Thr Leu Val Met Thr Arg Pro Ile Lys Gly Pro Arg Glu Ile
130                 405                 410                 415
132 cag ctg gac ttg gaa atg atc act gtc aac act gtc atc aac ttc aga     1296
133 Gln Leu Asp Leu Glu Met Ile Thr Val Asn Thr Val Ile Asn Phe Arg
134             420                 425                 430
136 ggc agc tcc gtg atc cga ctg cgg ata tat gtg tcg cag tac cca ttc     1344
137 Gly Ser Ser Val Ile Arg Leu Arg Ile Tyr Val Ser Gln Tyr Pro Phe
138         435                 440                 445
140 tga             1347
144 <210> SEQ ID NO: 2
145 <211> LENGTH: 448
146 <212> TYPE: PRT
147 <213> ORGANISM: Homo sapiens
149 <400> SEQUENCE: 2
151 Met Pro Gly Ile Lys Arg Ile Leu Thr Val Thr Ile Leu Ala Leu Cys
152 1               5                   10                  15
155 Leu Pro Ser Pro Gly Asn Ala Gln Ala Gln Cys Thr Asn Gly Phe Asp
156             20                  25                  30
159 Leu Asp Arg Gln Ser Gly Gln Cys Leu Asp Ile Asp Glu Cys Arg Thr
160         35                  40                  45
163 Ile Pro Glu Ala Cys Arg Gly Asp Met Met Cys Val Asn Gln Asn Gly
164     50                  55                  60
167 Gly Tyr Leu Cys Ile Pro Arg Thr Asn Pro Val Tyr Arg Gly Pro Tyr
168 65                  70                  75                  80
171 Ser Asn Pro Tyr Ser Thr Pro Tyr Ser Gly Pro Tyr Pro Ala Ala Ala
172                 85                  90                  95
175 Pro Pro Leu Ser Ala Pro Asn Tyr Pro Thr Ile Ser Arg Pro Leu Ile
176             100                 105                 110
179 Cys Arg Phe Gly Tyr Gln Met Asp Glu Ser Asn Gln Cys Val Asp Val
180         115                 120                 125
183 Asp Glu Cys Ala Thr Asp Ser His Gln Cys Asn Pro Thr Gln Ile Cys
184     130                 135                 140
187 Ile Asn Thr Glu Gly Gly Tyr Thr Cys Ser Cys Thr Asp Gly Tyr Trp
188 145                 150                 155                 160
191 Leu Leu Glu Gly Gln Cys Leu Asp Ile Asp Glu Cys Arg Tyr Gly Tyr
192                 165                 170                 175
195 Cys Gln Gln Leu Cys Ala Asn Val Pro Gly Ser Tyr Ser Cys Thr Cys
196             180                 185                 190
199 Asn Pro Gly Phe Thr Leu Asn Glu Asp Gly Arg Ser Cys Gln Asp Val
200         195                 200                 205
203 Asn Glu Cys Ala Thr Glu Asn Pro Cys Val Gln Thr Cys Val Asn Thr
204     210                 215                 220
207 Tyr Gly Ser Phe Ile Cys Arg Cys Asp Pro Gly Tyr Glu Leu Glu Glu
208 225                 230                 235                 240
211 Asp Gly Val His Cys Ser Asp Met Asp Glu Cys Ser Phe Ser Glu Phe
212                 245                 250                 255
215 Leu Cys Gln His Glu Cys Val Asn Gln Pro Gly Thr Tyr Phe Cys Ser
```

RAW SEQUENCE LISTING DATE: 10/13/2006
PATENT APPLICATION: US/10/594,339 TIME: 15:00:13

Input Set : A:\pto.da.txt
Output Set: N:\CRF4\10132006\J594339.raw

```
216                 260                 265                 270
219 Cys Pro Pro Gly Tyr Ile Leu Leu Asp Asp Asn Arg Ser Cys Gln Asp
220         275                 280                 285
223 Ile Asn Glu Cys Glu His Arg Asn His Thr Cys Asn Leu Gln Gln Thr
224     290                 295                 300
227 Cys Tyr Asn Leu Gln Gly Gly Phe Lys Cys Ile Asp Pro Ile Arg Cys
228 305                 310                 315                 320
231 Glu Glu Pro Tyr Leu Arg Ile Ser Asp Asn Arg Cys Met Cys Pro Ala
232                 325                 330                 335
235 Glu Asn Pro Gly Cys Arg Asp Gln Pro Phe Thr Ile Leu Tyr Arg Asp
236             340                 345                 350
239 Met Asp Val Val Ser Gly Arg Ser Val Pro Ala Asp Ile Phe Gln Met
240         355                 360                 365
243 Gln Ala Thr Thr Arg Tyr Pro Gly Ala Tyr Tyr Ile Phe Gln Ile Lys
244     370                 375                 380
247 Ser Gly Asn Glu Gly Arg Glu Phe Tyr Met Arg Gln Thr Gly Pro Ile
248 385                 390                 395                 400
251 Ser Ala Thr Leu Val Met Thr Arg Pro Ile Lys Gly Pro Arg Glu Ile
252                 405                 410                 415
255 Gln Leu Asp Leu Glu Met Ile Thr Val Asn Thr Val Ile Asn Phe Arg
256             420                 425                 430
259 Gly Ser Ser Val Ile Arg Leu Arg Ile Tyr Val Ser Gln Tyr Pro Phe
260         435                 440                 445
263 <210> SEQ ID NO: 3
264 <211> LENGTH: 1278
265 <212> TYPE: DNA
266 <213> ORGANISM: Homo sapiens
269 <220> FEATURE:
270 <221> NAME/KEY: CDS
271 <222> LOCATION: (1)..(1278)
273 <400> SEQUENCE: 3
274 cag gca cag tgc acg aat ggc ttt gac ctg gat cgc cag tca gga cag      48
275 Gln Ala Gln Cys Thr Asn Gly Phe Asp Leu Asp Arg Gln Ser Gly Gln
276 1               5                   10                  15
278 tgt tta gat att gat gaa tgc cga acc atc ccc gag gcc tgc cga gga      96
279 Cys Leu Asp Ile Asp Glu Cys Arg Thr Ile Pro Glu Ala Cys Arg Gly
280             20                  25                  30
282 gac atg atg tgt gtt aac caa aat ggc ggg tat tta tgc att ccc cgg     144
283 Asp Met Met Cys Val Asn Gln Asn Gly Gly Tyr Leu Cys Ile Pro Arg
284         35                  40                  45
286 aca aac cct gtg tat cga ggg ccc tac tcg aac ccc tac tcg acc ccc     192
287 Thr Asn Pro Val Tyr Arg Gly Pro Tyr Ser Asn Pro Tyr Ser Thr Pro
288     50                  55                  60
290 tac tca ggt ccg tac cca gca gct gcc cca cca ctc tca gct cca aac     240
291 Tyr Ser Gly Pro Tyr Pro Ala Ala Ala Pro Pro Leu Ser Ala Pro Asn
292 65                  70                  75                  80
294 tat ccc acg atc tcc agg cct ctt ata tgc cgc ttt gga tac cag atg     288
295 Tyr Pro Thr Ile Ser Arg Pro Leu Ile Cys Arg Phe Gly Tyr Gln Met
296                 85                  90                  95
```

RAW SEQUENCE LISTING DATE: 10/13/2006
PATENT APPLICATION: **US/10/594,339** TIME: 15:00:13

Input Set : **A:\pto.da.txt**
Output Set: **N:\CRF4\10132006\J594339.raw**

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298 gat gaa agc aac caa tgt gtg gat gtg gac gag tgt gca aca gat tcc      336
299 Asp Glu Ser Asn Gln Cys Val Asp Val Asp Glu Cys Ala Thr Asp Ser
300             100                 105                 110
302 cac cag tgc aac ccc acc cag atc tgc atc aat act gaa ggc ggg tac      384
303 His Gln Cys Asn Pro Thr Gln Ile Cys Ile Asn Thr Glu Gly Gly Tyr
304         115                 120                 125
306 acc tgc tcc tgc acc gac gga tat tgg ctt ctg gaa ggc cag tgc tta      432
307 Thr Cys Ser Cys Thr Asp Gly Tyr Trp Leu Leu Glu Gly Gln Cys Leu
308     130                 135                 140
310 gac att gat gaa tgt cgc tat ggt tac tgc cag cag ctc tgt gcg aat      480
311 Asp Ile Asp Glu Cys Arg Tyr Gly Tyr Cys Gln Gln Leu Cys Ala Asn
312 145                 150                 155                 160
314 gtt cct gga tcc tat tct tgt aca tgc aac cct ggt ttt acc ctc aat      528
315 Val Pro Gly Ser Tyr Ser Cys Thr Cys Asn Pro Gly Phe Thr Leu Asn
316                 165                 170                 175
318 gag gat gga agg tct tgc caa gat gtg aac gag tgt gcc acc gag aac      576
319 Glu Asp Gly Arg Ser Cys Gln Asp Val Asn Glu Cys Ala Thr Glu Asn
320             180                 185                 190
322 ccc tgc gtg caa acc tgc gtc aac acc tac ggc tct ttc atc tgc cgc      624
323 Pro Cys Val Gln Thr Cys Val Asn Thr Tyr Gly Ser Phe Ile Cys Arg
324         195                 200                 205
326 tgt gac cca gga tat gaa ctt gag gaa gat ggc gtt cat tgc agt gat      672
327 Cys Asp Pro Gly Tyr Glu Leu Glu Glu Asp Gly Val His Cys Ser Asp
328     210                 215                 220
330 atg gac gag tgc agc ttc tct gag ttc ctc tgc caa cat gag tgt gtg      720
331 Met Asp Glu Cys Ser Phe Ser Glu Phe Leu Cys Gln His Glu Cys Val
332 225                 230                 235                 240
334 aac cag ccc ggc aca tac ttc tgc tcc tgc cct cca ggc tac atc ctg      768
335 Asn Gln Pro Gly Thr Tyr Phe Cys Ser Cys Pro Pro Gly Tyr Ile Leu
336                 245                 250                 255
338 ctg gat gac aac cga agc tgc caa gac atc aac gaa tgt gag cac agg      816
339 Leu Asp Asp Asn Arg Ser Cys Gln Asp Ile Asn Glu Cys Glu His Arg
340             260                 265                 270
342 aac cac acg tgc aac ctg cag cag acg tgc tac aat tta caa ggg ggc      864
343 Asn His Thr Cys Asn Leu Gln Gln Thr Cys Tyr Asn Leu Gln Gly Gly
344         275                 280                 285
346 ttc aaa tgc atc gac ccc atc cgc tgt gag gag cct tat ctg agg atc      912
347 Phe Lys Cys Ile Asp Pro Ile Arg Cys Glu Glu Pro Tyr Leu Arg Ile
348     290                 295                 300
350 agt gat aac cgc tgt atg tgt cct gct gag aac cct ggc tgc aga gac      960
351 Ser Asp Asn Arg Cys Met Cys Pro Ala Glu Asn Pro Gly Cys Arg Asp
352 305                 310                 315                 320
354 cag ccc ttt acc atc ttg tac cgg gac atg gac gtg gtg tca gga cgc     1008
355 Gln Pro Phe Thr Ile Leu Tyr Arg Asp Met Asp Val Val Ser Gly Arg
356                 325                 330                 335
358 tcc gtt ccc gct gac atc ttc caa atg caa gcc acg acc cgc tac cct     1056
359 Ser Val Pro Ala Asp Ile Phe Gln Met Gln Ala Thr Thr Arg Tyr Pro
360             340                 345                 350
362 ggg gcc tat tac att ttc cag atc aaa tct ggg aat gag ggc aga gaa     1104
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RAW SEQUENCE LISTING ERROR SUMMARY DATE: 10/13/2006
PATENT APPLICATION: **US/10/594,339** TIME: 15:00:14

Input Set : **A:\pto.da.txt**
Output Set: **N:\CRF4\10132006\J594339.raw**

Invalid Line Length:
The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:1; Line(s) 140

Invalid <213> Response:
Use of "Artificial" only as "<213> Organism" response is incomplete, per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:17,18,19,20,21,22,23,24,25,26,27,28,29

VERIFICATION SUMMARY DATE: 10/13/2006
PATENT APPLICATION: **US/10/594,339** TIME: 15:00:14

Input Set : **A:\pto.da.txt**
Output Set: **N:\CRF4\10132006\J594339.raw**

L:8 M:201 W: Mandatory field data missing, <130> FILE REFERENCE
L:10 M:270 C: Current Application Number differs, Replaced Current Application No
L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:11 M:256 W: Invalid Numeric Header Field, Wrong Prior FILING DATE:YYYY-MM-DD

Raw Sequence Listing before editing,
for reference only

IFWP

RAW SEQUENCE LISTING DATE: 10/10/2006
PATENT APPLICATION: **US/10/594,339** TIME: 14:53:44

Input Set : **A:\Sequence Listing 2006-1605A.txt**
Output Set: **N:\CRF4\10102006\J594339.raw**

3 <110> APPLICANT: Kyoto University
5 <120> TITLE OF INVENTION: Cleaved forms of DANCE and DANCE complexes, and methods of screening
6 an agent for regulating formation of elastic fibre using them
W--> 8 <130> FILE REFERENCE:
C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/594,339
C--> 10 <141> CURRENT FILING DATE: 2006-09-27
10 <150> PRIOR APPLICATION NUMBER: JP 2004-096685
W--> 11 <151> PRIOR FILING DATE: 2004-3-29
13 <160> NUMBER OF SEQ ID NOS: 29
15 <170> SOFTWARE: PatentIn version 3.2

Does Not Comply
Corrected Diskette Needed
(Pg-3)

ERRORED SEQUENCES

17 <210> SEQ ID NO: 1
18 <211> LENGTH: 1347
19 <212> TYPE: DNA
20 <213> ORGANISM: Homo sapiens
23 <220> FEATURE:
24 <221> NAME/KEY: CDS
25 <222> LOCATION: (1)..(1347)
27 <400> SEQUENCE: 1

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28 atg cca gga ata aaa agg ata ctc act gtt acc att ctg gct ctc tgt       48
29 Met Pro Gly Ile Lys Arg Ile Leu Thr Val Thr Ile Leu Ala Leu Cys
30 1               5                  10                  15
32 ctt cca agc cct ggg aat gca cag gca cag tgc acg aat ggc ttt gac       96
33 Leu Pro Ser Pro Gly Asn Ala Gln Ala Gln Cys Thr Asn Gly Phe Asp
34             20                  25                  30
36 ctg gat cgc cag tca gga cag tgt tta gat att gat gaa tgc cga acc      144
37 Leu Asp Arg Gln Ser Gly Gln Cys Leu Asp Ile Asp Glu Cys Arg Thr
38         35                  40                  45
40 atc ccc gag gcc tgc cga gga gac atg atg tgt gtt aac caa aat ggc      192
41 Ile Pro Glu Ala Cys Arg Gly Asp Met Met Cys Val Asn Gln Asn Gly
42     50                  55                  60
44 ggg tat tta tgc att ccc cgg aca aac cct gtg tat cga ggg ccc tac      240
45 Gly Tyr Leu Cys Ile Pro Arg Thr Asn Pro Val Tyr Arg Gly Pro Tyr
46 65                  70                  75                  80
48 tcg aac ccc tac tcg acc ccc tac tca ggt ccg tac cca gca gct gcc      288
49 Ser Asn Pro Tyr Ser Thr Pro Tyr Ser Gly Pro Tyr Pro Ala Ala Ala
50                 85                  90                  95
52 cca cca ctc tca gct cca aac tat ccc acg atc tcc agg cct ctt ata      336
53 Pro Pro Leu Ser Ala Pro Asn Tyr Pro Thr Ile Ser Arg Pro Leu Ile
54             100                 105                 110
```

RAW SEQUENCE LISTING DATE: 10/10/2006
PATENT APPLICATION: **US/10/594,339** TIME: 14:53:44

Input Set : **A:\Sequence Listing 2006-1605A.txt**
Output Set: **N:\CRF4\10102006\J594339.raw**

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56 tgc cgc ttt gga tac cag atg gat gaa agc aac caa tgt gtg gat gtg      384
57 Cys Arg Phe Gly Tyr Gln Met Asp Glu Ser Asn Gln Cys Val Asp Val
58         115                 120                 125
60 gac gag tgt gca aca gat tcc cac cag tgc aac ccc acc cag atc tgc      432
61 Asp Glu Cys Ala Thr Asp Ser His Gln Cys Asn Pro Thr Gln Ile Cys
62     130                 135                 140
64 atc aat act gaa ggc ggg tac acc tgc tcc tgc acc gac gga tat tgg      480
65 Ile Asn Thr Glu Gly Gly Tyr Thr Cys Ser Cys Thr Asp Gly Tyr Trp
66 145                 150                 155                 160
68 ctt ctg gaa ggc cag tgc tta gac att gat gaa tgt cgc tat ggt tac      528
69 Leu Leu Glu Gly Gln Cys Leu Asp Ile Asp Glu Cys Arg Tyr Gly Tyr
70                 165                 170                 175
72 tgc cag cag ctc tgt gcg aat gtt cct gga tcc tat tct tgt aca tgc      576
73 Cys Gln Gln Leu Cys Ala Asn Val Pro Gly Ser Tyr Ser Cys Thr Cys
74             180                 185                 190
76 aac cct ggt ttt acc ctc aat gag gat gga agg tct tgc caa gat gtg      624
77 Asn Pro Gly Phe Thr Leu Asn Glu Asp Gly Arg Ser Cys Gln Asp Val
78         195                 200                 205
80 aac gag tgt gcc acc gag aac ccc tgc gtg caa acc tgc gtc aac acc      672
81 Asn Glu Cys Ala Thr Glu Asn Pro Cys Val Gln Thr Cys Val Asn Thr
82     210                 215                 220
84 tac ggc tct ttc atc tgc cgc tgt gac cca gga tat gaa ctt gag gaa      720
85 Tyr Gly Ser Phe Ile Cys Arg Cys Asp Pro Gly Tyr Glu Leu Glu Glu
86 225                 230                 235                 240
88 gat ggc gtt cat tgc agt gat atg gac gag tgc agc ttc tct gag ttc      768
89 Asp Gly Val His Cys Ser Asp Met Asp Glu Cys Ser Phe Ser Glu Phe
90                 245                 250                 255
92 ctc tgc caa cat gag tgt gtg aac cag ccc ggc aca tac ttc tgc tcc      816
93 Leu Cys Gln His Glu Cys Val Asn Gln Pro Gly Thr Tyr Phe Cys Ser
94             260                 265                 270
96 tgc cct cca ggc tac atc ctg ctg gat gac aac cga agc tgc caa gac      864
97 Cys Pro Pro Gly Tyr Ile Leu Leu Asp Asp Asn Arg Ser Cys Gln Asp
98         275                 280                 285
100 atc aac gaa tgt gag cac agg aac cac acg tgc aac ctg cag cag acg      912
101 Ile Asn Glu Cys Glu His Arg Asn His Thr Cys Asn Leu Gln Gln Thr
102     290                 295                 300
104 tgc tac aat tta caa ggg ggc ttc aaa tgc atc gac ccc atc cgc tgt      960
105 Cys Tyr Asn Leu Gln Gly Gly Phe Lys Cys Ile Asp Pro Ile Arg Cys
106 305                 310                 315                 320
108 gag gag cct tat ctg agg atc agt gat aac cgc tgt atg tgt cct gct     1008
109 Glu Glu Pro Tyr Leu Arg Ile Ser Asp Asn Arg Cys Met Cys Pro Ala
110                 325                 330                 335
112 gag aac cct ggc tgc aga gac cag ccc ttt acc atc ttg tac cgg gac     1056
113 Glu Asn Pro Gly Cys Arg Asp Gln Pro Phe Thr Ile Leu Tyr Arg Asp
114             340                 345                 350
116 atg gac gtg gtg tca gga cgc tcc gtt ccc gct gac atc ttc caa atg     1104
117 Met Asp Val Val Ser Gly Arg Ser Val Pro Ala Asp Ile Phe Gln Met
118         355                 360                 365
120 caa gcc acg acc cgc tac cct ggg gcc tat tac att ttc cag atc aaa     1152
```

RAW SEQUENCE LISTING DATE: 10/10/2006
PATENT APPLICATION: **US/10/594,339** TIME: 14:53:44

Input Set : **A:\Sequence Listing 2006-1605A.txt**
Output Set: **N:\CRF4\10102006\J594339.raw**

```
121 Gln Ala Thr Thr Arg Tyr Pro Gly Ala Tyr Tyr Ile Phe Gln Ile Lys
122     370                 375                 380
124 tct ggg aat gag ggc aga gaa ttt tac atg cgg caa acg ggc ccc atc     1200
125 Ser Gly Asn Glu Gly Arg Glu Phe Tyr Met Arg Gln Thr Gly Pro Ile
126 385                 390                 395                 400
128 agt gcc acc ctg gtg atg aca cgc ccc atc aaa ggg ccc cgg gaa atc     1248
129 Ser Ala Thr Leu Val Met Thr Arg Pro Ile Lys Gly Pro Arg Glu Ile
130                 405                 410                 415
132 cag ctg gac ttg gaa atg atc act gtc aac act gtc atc aac ttc aga     1296
133 Gln Leu Asp Leu Glu Met Ile Thr Val Asn Thr Val Ile Asn Phe Arg
134             420                 425                 430
136 ggc agc tcc gtg atc cga ctg cgg ata tat gtg tcg cag tac cca ttc     1344
137 Gly Ser Ser Val Ile Arg Leu Arg Ile Tyr Val Ser Gln Tyr Pro Phe
138         435                 440                 445
E--> 140 tga
141 1347
```

1347

RAW SEQUENCE LISTING ERROR SUMMARY DATE: 10/10/2006
PATENT APPLICATION: **US/10/594,339** TIME: 14:53:46

Input Set : **A:\Sequence Listing 2006-1605A.txt**
Output Set: **N:\CRF4\10102006\J594339.raw**

Invalid <213> Response:
Use of "Artificial" only as "<213> Organism" response is incomplete, per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:17,18,19,20,21,22,23,24,25,26,27,28,29

VERIFICATION SUMMARY DATE: 10/10/2006
PATENT APPLICATION: **US/10/594,339** TIME: 14:53:46

Input Set : **A:\Sequence Listing 2006-1605A.txt**
Output Set: **N:\CRF4\10102006\J594339.raw**

L:8 M:201 W: Mandatory field data missing, <130> FILE REFERENCE
L:10 M:270 C: Current Application Number differs, Replaced Current Application No
L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:11 M:256 W: Invalid Numeric Header Field, Wrong Prior FILING DATE:YYYY-MM-DD
L:140 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:1347 SEQ:1